

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/679,366
Source: 1FWS
Date Processed by STIC: 10/21/2003

ENTERED



IFWO

RAW SEQUENCE LISTING

DATE: 10/21/2003

PATENT APPLICATION: US/10/679,366

TIME: 14:49:12

Input Set : E:\AM101072(US).ST25.txt

Output Set: N:\CRF4\10212003\J679366.raw

3 <110> APPLICANT: Liu, Wei

4 Wu, Leeying

6 <120> TITLE OF INVENTION: COMPOSITIONS, ORGANISMS AND METHODOLOGIES EMPLOYING A NOVEL

HUMAN

7 KINASE

9 <130> FILE REFERENCE: AM101072

C--> 11 <140> CURRENT APPLICATION NUMBER: US/10/679,366

C--> 11 <141> CURRENT FILING DATE: 2003-10-07

11 <160> NUMBER OF SEQ ID NOS: 168

13 <170> SOFTWARE: PatentIn version 3.2

15 <210> SEQ ID NO: 1

16 <211> LENGTH: 5199

17 <212> TYPE: DNA

18 <213> ORGANISM: Homo sapiens

20 <400> SEQUENCE: 1

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39	tacttggtcg	agatggtgat	agcaattgac	tcagttcatc	agctacatta	tgtacacaga	600
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83	ctgcgagaa	cagaaagagc	caaaaaagag	gttagtattc	atacagaagc	tctagctgct	1920
85	gaagcatcta	aagacaggaa	gctacgtgaa	cagagtgagc	actattctaa	gcaactggaa	1980
87	aatgaattgg	agggaactgaa	gcaaaaacaa	attagttact	caccaggagt	atgcagcata	2040
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91	gaagaagaat	tatctaaaag	agaaggaata	catgcaaatg	aaataaaaaa	tcttaagaaa	2160
93	gaactgcatg	attcagaagg	tcagcaactt	gctctcaaca	aagaaattat	gattttaaaa	2220
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208 20 25 30
211 Asp Ile Leu Ile Cys Leu Tyr Asp Glu Cys Asn Asn Ser Pro Leu Arg
212 35 40 45
215 Arg Glu Lys Asn Ile Leu Glu Tyr Leu Glu Trp Ala Lys Pro Phe Thr
216 50 55 60
219 Ser Lys Val Lys Gln Met Arg Leu His Arg Glu Asp Phe Glu Ile Leu
220 65 70 75 80
223 Lys Val Ile Gly Arg Gly Ala Phe Gly Glu Val Ala Val Val Lys Leu
224 85 90 95
227 Lys Asn Ala Asp Lys Val Phe Ala Met Lys Ile Leu Asn Lys Trp Glu
228 100 105 110
231 Met Leu Lys Arg Ala Glu Thr Ala Cys Phe Arg Glu Glu Arg Asp Val
232 115 120 125
235 Leu Val Asn Gly Asp Asn Lys Trp Ile Thr Thr Leu His Tyr Ala Phe
236 130 135 140
239 Gln Asp Asp Asn Asn Leu Tyr Leu Val Met Asp Tyr Tyr Val Gly Gly
240 145 150 155 160
243 Asp Leu Leu Thr Leu Leu Ser Lys Phe Glu Asp Arg Leu Pro Glu Asp
244 165 170 175
247 Met Ala Arg Phe Tyr Leu Ala Glu Met Val Ile Ala Ile Asp Ser Val
248 180 185 190
251 His Gln Leu His Tyr Val His Arg Asp Ile Lys Pro Asp Asn Ile Leu
252 195 200 205
255 Met Asp Met Asn Gly His Ile Arg Leu Ala Asp Phe Gly Ser Cys Leu
256 210 215 220
259 Lys Leu Met Glu Asp Gly Thr Val Gln Ser Ser Val Ala Val Gly Thr
260 225 230 235 240
263 Pro Asp Tyr Ile Ser Pro Glu Ile Leu Gln Ala Met Glu Asp Gly Lys
264 245 250 255
267 Gly Arg Tyr Gly Pro Glu Cys Asp Trp Trp Ser Leu Gly Val Cys Met
268 260 265 270
271 Tyr Glu Met Leu Tyr Gly Glu Thr Pro Phe Tyr Ala Glu Ser Leu Val

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276 290	295	300	
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283 Leu Ile Cys Ser Arg Glu His Arg Leu Gly Gln Asn Gly Ile Glu Asp			
284 325	330	335	
287 Phe Lys Lys His Pro Phe Phe Ser Gly Ile Asp Trp Asp Asn Ile Arg			
288 340	345	350	
291 Asn Cys Glu Ala Pro Tyr Ile Pro Glu Val Ser Ser Pro Thr Asp Thr			
292 355	360	365	
295 Ser Asn Phe Asp Val Asp Asp Cys Leu Lys Asn Ser Glu Thr Met			
296 370	375	380	
299 Pro Pro Pro Thr His Thr Ala Phe Ser Gly His His Leu Pro Phe Val			
300 385	390	395	400
303 Gly Phe Thr Tyr Thr Ser Ser Cys Val Leu Ser Asp Arg Ser Cys Leu			
304 405	410	415	
307 Arg Val Thr Ala Gly Pro Thr Ser Leu Asp Leu Asp Val Asn Val Gln			
308 420	425	430	
311 Arg Thr Leu Asp Asn Asn Leu Ala Thr Glu Ala Tyr Glu Arg Arg Ile			
312 435	440	445	
315 Lys Arg Leu Glu Gln Glu Lys Leu Glu Leu Ser Arg Lys Leu Gln Glu			
316 450	455	460	
319 Ser Thr Gln Thr Val Gln Ala Leu Gln Tyr Ser Thr Val Asp Gly Pro			
320 465	470	475	480
323 Leu Thr Ala Ser Lys Asp Leu Glu Ile Lys Asn Leu Lys Glu Glu Ile			
324 485	490	495	
327 Glu Lys Leu Arg Lys Gln Val Thr Glu Ser Ser His Leu Glu Gln Gln			
328 500	505	510	
331 Leu Glu Glu Ala Asn Ala Val Arg Gln Glu Leu Asp Asp Ala Phe Arg			
332 515	520	525	
335 Gln Ile Lys Ala Tyr Glu Lys Gln Ile Lys Thr Leu Gln Gln Glu Arg			
336 530	535	540	
339 Glu Asp Leu Asn Lys Glu Leu Val Gln Ala Ser Glu Arg Leu Lys Asn			
340 545	550	555	560
343 Gln Ser Lys Glu Leu Lys Asp Ala His Cys Gln Arg Lys Leu Ala Met			
344 565	570	575	
347 Gln Glu Phe Met Glu Ile Asn Glu Arg Leu Thr Glu Leu His Thr Gln			
348 580	585	590	
351 Lys Gln Lys Leu Ala Arg His Val Arg Asp Lys Glu Glu Glu Val Asp			
352 595	600	605	
355 Leu Val Met Gln Lys Val Glu Ser Leu Arg Gln Glu Leu Arg Arg Thr			
356 610	615	620	
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360 625	630	635	640
363 Glu Ala Ser Lys Asp Arg Lys Leu Arg Glu Gln Ser Glu His Tyr Ser			
364 645	650	655	
367 Lys Gln Leu Glu Asn Glu Leu Glu Gly Leu Lys Gln Lys Gln Ile Ser			
368 660	665	670	

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379 Ser Lys Arg Glu Gly Ile His Ala Asn Glu Ile Lys Asn Leu Lys Lys
380 705          710          715          720
383 Glu Leu His Asp Ser Glu Gly Gln Gln Leu Ala Leu Asn Lys Glu Ile
384          725          730          735
387 Met Ile Leu Lys Asp Lys Leu Glu Lys Thr Arg Arg Glu Ser Gln Ser
388          740          745          750
391 Glu Arg Glu Glu Phe Glu Ser Glu Phe Lys Gln Gln Tyr Glu Arg Glu
392          755          760          765
395 Lys Val Leu Leu Thr Glu Glu Asn Lys Lys Leu Thr Ser Glu Leu Asp
396          770          775          780
399 Lys Leu Thr Thr Leu Tyr Glu Asn Leu Ser Ile His Asn Gln Gln Leu
400 785          790          795          800
403 Glu Glu Glu Val Lys Asp Leu Ala Asp Lys Lys Glu Ser Val Ala His
404          805          810          815
407 Trp Glu Ala Gln Ile Thr Glu Ile Ile Gln Trp Val Ser Asp Glu Lys
408          820          825          830
411 Asp Ala Arg Gly Tyr Leu Gln Ala Leu Ala Ser Lys Met Thr Glu Glu
412          835          840          845
415 Leu Glu Ala Leu Arg Asn Ser Ser Leu Gly Thr Arg Ala Thr Asp Met
416          850          855          860
419 Pro Trp Lys Met Arg Arg Phe Ala Lys Leu Asp Met Ser Ala Arg Leu
420 865          870          875          880
423 Glu Leu Gln Ser Ala Leu Asp Ala Glu Ile Arg Ala Lys Gln Ala Ile
424          885          890          895
427 Gln Glu Glu Leu Asn Lys Val Lys Ala Ser Asn Ile Ile Thr Glu Cys
428          900          905          910
431 Lys Leu Lys Asp Ser Glu Lys Lys Asn Leu Glu Leu Leu Ser Glu Ile
432          915          920          925
435 Glu Gln Leu Ile Lys Asp Thr Glu Glu Leu Arg Ser Glu Lys Gly Ile
436          930          935          940
439 Glu His Gln Asp Ser Gln His Ser Phe Leu Ala Phe Leu Asn Thr Pro
440 945          950          955          960
443 Thr Asp Ala Leu Asp Gln Phe Glu Arg Ser Pro Ser Cys Thr Pro Ala
444          965          970          975
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452          995          1000          1005
455 Lys Arg Lys Thr His Gln Phe Phe Val Lys Ser Phe Thr Thr Pro
456          1010          1015          1020
459 Thr Lys Cys His Gln Cys Thr Ser Leu Met Val Gly Leu Ile Arg
460          1025          1030          1035
463 Gln Gly Cys Ser Cys Glu Val Cys Gly Phe Ser Cys His Ile Thr
464          1040          1045          1050
467 Cys Val Asn Lys Ala Pro Thr Thr Cys Pro Val Pro Pro Glu Gln

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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

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VERIFICATION SUMMARY

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L:11 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:2044 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3 after pos.:41280
M:341 Repeated in SeqNo=3